

FIGURE 1-2

1361 gtacggattcgggaccccgatccccgcccatagtgtaatggctcaactgccaaagtcagcattggaccgaaaattattggac 1440  
 1441 acgaagtactaatgtgaaaaaactttacatttggttattttctactttaataactatgctattttcaaaatttgaactttaat 1520  
 1521 actatgtttttatatagtttagtatatcttaatttttatgcaaaattcatctaattgtattaaactatttttcgatccgtag 1600  
 1601 ctaattatttcgaaggcaagtc aaagtgttattgttgactatgtgagctaattattgaacctttatctctcccaaccactc 1680  
 1681 aagttaattgaaccaaactcgatcgggttggttcgagctattttcgagccattgtgttatatgcacgtgagatatcaag 1760  
 1761 attgaccggaacactttatttatgataatgtagaaaaaagaaacatatattctaagactacatgcatgcaaaagtgc aaccctt 1840  
 1841 gcatgaaagctgctcaacacgtggcatagactcccgccacgtgtccattccacctcatccctcaccctcccccaccgtttcac 1920  
 1921 ctcttattatcacaaacaatcaatcaatcctactcctccatactcgaacaaatccgaccaacttataccaatattccca 2000  
 2001 aacttgattaatttctcagcaat ATG GAT CAG ACG CAC CAG ACA TAC GCC GGA ACC ACG CAG AAC 2065  
 1 M D Q T H Q T Y A G T T Q N 14  
 2066 CCG AGC TAT GGC GGC GGC ACA ATG TAG CAG CAG CAG CCG AGG TCT TAC CAG GCG 2125  
 15 P S Y G G G T M Y Q Q Q P R S Y Q A 34  
 2126 GTG AAG GCG GCC ACT GCA GCC ACC GCG GGT GGA TCC CTC ATC GTT CTG TCC GGT CTC ATC 2185  
 35 V K A A T A A T A G G S L I V L S G L I 54  
 2186 CTT ACG GCC ACC GTC ATT TCA CTC ATC ATA GCC ACC CCT CTC CTT GTC ATC TTC AGC CCT 2245  
 55 L T A T V I S L I A T P L L V I F S P 74  
 2246 GTT CTT GTC CCG GCT CTC ATC ACC GTC GGC CTC TTG ATC ACC GGG TTT CTT GCT TCC GGT 2305  
 75 V L V P A L I T V G L L I T G F L A S G 94  
 2306 GGG TTC GGA GTC GCC GGC GTC ACC GTC TTG TCC TGG ATC TAT AG gtagtataagctttggactt 2370  
 95 G F G V A A V T V L S W I Y R 109  
 2371 tagtattgtataaaatacataaagctgatttatgaacatggatctcccaacaagaggttatttaaatgcattctcgtctg 2450

FIGURE 1-3

2451 actcgatcggtgtgtttgagctactcgtgcacaatggtcgggtcggtctctggatctgttataataatttggaaagcc 2530  
 2531 tgaagtttcattgttctgccccaaacttcccactaccttttgagggtgttaagaagccatacaaaactaattatgaatccct 2610  
 2611 cccaaactcagaactcgagtcagtggtgtgacggttctctataaaacatttcgaaaaatctttgttccaatgaacgtag 2690  
 2691 aaatgaccatgcttgatgattgtgggtcttataag G TAC GTG ACC GGC GGG CAC CCG GCG GGA GGG 2756  
 110 Y V T G G G H P A G G  
 2757 GAT TCG CTG GAC CAG GCT AGG TCG AAG CTG GCC GGA AAG GCC AGG GAG GTG AAG GAC AGG 2816  
 120 D S L D Q A R S K L A G K A R E V K D R 139  
 2817 GCG TCG GAG TTC GCA CAG CAG CAT GTC ACA GGT GGT CAA CAG ACC TCT TAA agagagtcctct 2879  
 140 A S E F A Q Q H V T G G Q Q T S \* 156  
 2880 agttaaattggtcttctgtttctgtttcgtggcggttgtaaactctcttttaagtggtgctgttttccctttgtctcgtgt 2959  
 2960 gttgtaagtgaagtgaatcgaaagtcccaagttggagatgtttgttaacgatgatgttttctaaataatcagagatat 3039  
 3040 aaggggtgctaatttagtattgctgtctgatctcgcgaccacaaactcgaaagtaaaattgcagaggatgagttgtacagaaca 3119  
 3120 agcgtgcattgttctggaagttcatctccttggagccgaccttgttgcagtttcgccaagtcactagacaatggt 3199  
 3200 acgagttaagcctctgtcaaacagatcgctctagcgtcccagaaaaacaccagatttttcgaaaaaccatcggggatcaatt 3279  
 3280 ttcgattcaattccgatcttggaagtacttgaaacagaagcatgatgctaaaaagataataagaaaatcgaaagcctagaaaaag 3359  
 3360 ttgtacagaaagcaacaagtcaaaaaatatagatcaacttcaagggttcaaaattacatcttacagacccccaaaaaatgaca 3439  
 3440 gttaacagaagtcgactaaacagaaaaccagccagcttcacctgggaatgaaggagctttgatcaatcccatcctagcttcat 3519  
 3520 tcccccttgaaaattgcagacagagctctcatcctctgctaaaagctggtggcttattcttaacctgcaatcaataagcatga 3599  
 3600 actaacattggacaccttcacgcgggattgtctcgaaaatcagtgagcgggatttacctgtgtgtgtagtaaacctctc 3679

## FIGURE 1-4

3680 tccttgataaaatctggaaattccggcatcaactactgccacctttctgttaagtgattttatcaccaaggctga 3759  
3760 gcgtgattccttgctgtctccgaatcctgatgtatccactgagctttccatctccttctcctccaggccttatgttc 3839  
3840 accaatgcgtcctcgccgaacacacactcttgcggtacaaagttcgcagccagggaatccacactctccatcaagtgcagacct 3919  
3920 gcaaacccccaaataagaacacacaaactccaaaagtcacgatcaattctccgcctttttatgaagaaaaaggaaacttctgggt 3999  
4000 acttacgggtgccgtcagacacttcataattttagacttgatgatgtgtccagggaattccttctcgttctgaattgtgt 4079  
4080 gttaacagcaacctgacagacagaaagatatcgcaaatttaagatactgggatgactaggcacagagaaatgaaatcttaa 4159  
4160 ttctagaagtaaaaccttattttcccattcaaatctgtcccacatagtcgggaacgcagcatccgagcaagaagcaggag 4239  
4240 agatgtaatccatgatatcgatgtggatatcgttgaggacgacaaactgaacgttccatcacattgg 4305







FIGURE 3-1

```

1  tccactatgtaggtcataatccatcatcttttaatttttgggcaccattccaattccatcttgccttttagggatgtgaatatga  80
    5' primer (1)      AT rich
81  acggccaaggtaagagataataataatccaaattaaagcaagagagcccaagtaagataatccaaatgtacacttgtca  160
    AT rich
161  tcgccgaaattagtaaaatcgcggcatattgtattcccacacattattaaaataccgtatatgtattggctgcatttgc  240

241  atgaataatactacgtgttaagcccaaaagaaacccacgtgtagcccatgcaaaagttaacactcagcacccttcctcagt  320
    RY      G box seed-specific
321  ctccactatataaaacccaccatcccccaatcttacaaaacccaccacacgactcacaaactcgactctcacaccccttaaagaa  400
    TATA      3' primer (1)
401  ccaatcaccaccacaaaaaATGGCAAAGCTGATGAGCCTAGACCCCTAGCAACGCAAGTTCTCTTCTGATCGTGGTGGAC  480
    1      M A K L M S L A A V A T Q F L F L I V V D 21

481  GCATCCGTCCGAACCAACAGTGTATTATCGACGAGGAGACCAACCAAGCCGGGTGGAGGCAAGGTGGCAGGGACAGCAGC  560
22  A S V R T T V I I D E E T N Q G R G G K V A G T A A 48

561  AGTCTGCGAGCAGATCCAGCAGCGAGACTTCTTGAGGAGCTGCCAGCAGTTTCATGTGGGAGAAAAGTCCAGAGGGGCG  640
49  V C E Q Q I Q Q R D F L R S C Q Q F M W E K V Q R G G 75

641  GCCACAGCCACTATTACAACCAAGGGCCGTGGAGGAGGCGGAACAGAGCCAGTACTTCGAACAGCTGTTGTGACGACCTTA  720
76  H S H Y Y N Q G R G G G E Q S Q Y F E Q L F V T T L 101

721  AGCAATTGCGCACCGGGTGCACCATGCCAGGGGACTTGAAGCGTGCATCGGCCAAATGAGGCAGGAAATCCAGCAGCA  800
102  S N C A P R C T M P G D L K R A I G Q Q M R Q E I Q Q Q 128

801  GGGACAGCAGCAGGACAGCAGGAAGTTCAGAGGTGGATCCAGCAAGCTAAACAAATCGCTAAGGACCTCCCCGGAC  880
129  G Q Q Q Q Q Q Q E V Q R W I Q Q A K Q I A K D L P G Q 155

```





1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
ctgatatcccgctcatttgcatccacgtgcgcgcctcccgtgccaaagtcctagggtcatgcacgccaaattggtggtggtgcgggctgcctgtgctt									
ABRE									
1310	1320	1330	1340	1350	1360	1370	1380	1390	1400
cttaccgatgggtggaggttgagttgggggtctccgcgcgcgatggtagtgggttgacgggttgggtggtgacggcattgatcaatttacttcttgc									
R1									
1410	1420	1430	1440	1450	1460	1470	1480	1490	1500
ttcaaatctttggcagaaaaacaattcattagattagaactggaaccagagtgatgagacggattaaagtcagattccaacagagttacatctcttaaga									
R1									
1510	1520	1530	1540	1550	1560	1570	1580	1590	1600
aataatgtaaccccttagacttttatatttgcattaaaaataatttaacttttagactttatatatagttttaataactaaagtttaaccactcta									
R2									
1610	1620	1630	1640	1650	1660	1670	1680	1690	1700
ttatttatatgaaactatttgcctccctctaaataaacttggtattggtgtttacagaaccctataatcaataataactcaatactcaactgaagtttg									
1710	1720	1730	1740	1750	1760	1770	1780	1790	1800
tgcagttaattgaaggattaaacggccaaaatgcaactagttattatcaaccgaatagattcacactagatggccatttcccatcaatatcatcgccgttctt									
1810	1820	1830	1840	1850	1860	1870	1880	1890	1900
cttctgtccacatatcccctctgaaacttgagagacacctgcacttcattgtccttattacgtgttaaaaaatgaaccccatgcatccatgcacaaactgaa									
Legumin Vicilin									
1910	1920	1930	1940	1950	1960	1970	1980	1990	2000
gaatggcgcaagaaccttccctccatttcttatgtggcgaccatccatttcacatctccgcctataaaacaccccccatcacttcacctagaacatca									
CAAT									
2010	2020	2030	2040	2050	2060	2070	2080	2090	2100
tcactacttgcttatccatccaaaaagatacccaccatggctagatcatcaagcccttgccttctcactctgcattttgcgcatttcttccactcttc									
TATA									
Signal sequence									
2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
TCTGGGTAGGCAGCAATTCCACGAGGGGAACGACTGCCAGATCGACAGGATCGACGCATCCGAGCCGGACAAAACCATCCAGGCAGAGTGGCACCATC									
L G R Q Q F Q Q G N E C Q I D R I D A S E P D K T I Q A E A G T I									
2210	2220	2230	2240	2250	2260	2270	2280	2290	2300
GAGGTATGGACCAAGACCGCCAGCAATTCACGTGGCTGGTGTGCCGTGTGAAGCGGCACCATTCAGCCCAAAAGTCTTCTTCTGCTTCTACAGCA									
E V W D Q N R Q Q F Q C A G V A V R R T I E P K G L L L P F Y S									

FIGURE 4-3

2310 2320 2330 2340 2350 2360 2370 2380 2390 2400  
ACACCCCTCAGCTCATCTACATCGTTCAAGgtataaattaaatcagttcatacaaatgataaaccaccacttcgaatgtatttatcaaatatcaatgatcga  
N T P Q L I Y I V Q

2410 2420 2430 2440 2450 2460 2470 2480 2490 2500  
tgcacctgtatgtgtgtatattcagTAGGGGAGTTACAGGAATCATGTTCCKAKGATGTCCAGAGACATTCGAGGAATCCCAGCAGCAAGGACAAC  
G R G V T G I M F P X C P E T F E S Q Q Q G Q

2510 2520 2530 2540 2550 2560 2570 2580 2590 2600  
AGGGCCACACAGGGTAGTTCCCAAGACCAGCACCCAGATCCGCCGCTTCGGTGAAGGTGACGTCAATTGCCGTCCCTGCCGGTGTAGCCCACTGGTCCTA  
Q G Q Q G S S Q D Q H Q K I R R F R E G D V I A V P A G V A H W S Y

2610 2620 2630 2640 2650 2660 2670 2680 2690 2700  
CAACGATGGCAACGAACCAAGTCATGGCCATTGTTGTCCATGACACTTCCAGCCACCTCAACCAACTGGACAACAACCCAGGgtatataagcattgccgt  
N D G N E P V M A I V V H D T S S H L N Q L D N N P R

2710 2720 2730 2740 2750 2760 2770 2780 2790 2800  
agttgctaataaattgcacacaattggaactctatatttcagtatctaataacttttccctttttggcagAACTTCTACTTGGCAGGAACCCCGAGAGAC  
N F Y L A G N P R D

2810 2820 2830 2840 2850 2860 2870 2880 2890 2900  
GAGTTCGAACAATCGCAGCAAGGAGGCAGGCTGAGCCCTGGGGAGAGTGAAGGTGGACGAGGACGAGGGAACCTCTTCAACCTGCAACAACCTCTTCTT  
E F E Q S Q Q G G R L S R G E S E G G R G R E P L Q P A T T S S

2910 2920 2930 2940 2950 2960 2970 2980 2990 3000  
GCGGAATCGACTCCAAGCTCATCGCGGAGGCGTTCAATGTCCAGCAGAACGTGGCAAGGAGGTACAGAGCGAGAACGACAACAGAGGCCAGATCGTCCG  
C G I D S K L I A E A F N V D E N V A R R L Q S E N D N R G Q I V R

3010 3020 3030 3040 3050 3060 3070 3080 3090 3100  
AGTCGAAGCGCAGCTCGACATCGTCAGACCTCCGACCATCCAGAGGAGTCAAGGAGCAGGAGGCGTGGTGGTGGCCGCTACTACTCCAATGGA  
V E G E L D I V R P P T S I Q E E S Q E Q G G R G G G R Y Y S N G

3110 3120 3130 3140 3150 3160 3170 3180 3190 3200  
GTGGAGGAGACCTTCTGCTCCATGAGACTAATTGAGAACATCGGCGATCCTTCTCGGGCAGACATTTTCACTCCAGAGCGCGCGTGTAGATCCCTCA  
V E E T F C S M R L I E N I G D P S R A D I F T P E A G R V R S L

FIGURE 4-4

3210 3220 3230 3240 3250 3260 3270 3280 3290 3300  
 ACAGGCACAACCTCCCGGTCTGTGCAATGGATCCAGCTTAGCGCCGAGAGAGCGGTCTCTACAAATgtatagatctcactcagcaccaactctaaattga  
 N S H N L P V L Q W I Q L S A E R G V L Y N  
  
 3310 3320 3330 3340 3350 3360 3370 3380 3390 3400  
 atccctaattttaaattcaccgatattctgaccgacggtttgaatttttagGAAGCGATCAGGCTGCCGCACTGGAACATCAACGCACAGCATAGT  
 E A I R L P H W N I N A H S I V  
  
 3410 3420 3430 3440 3450 3460 3470 3480 3490 3500  
 GTACGGCATCAGAGGACAAGCCAGAGTCCAGATCGTGAACGAGGAAGGAATTCCGGTGTTCGATGGAGTGTGCAGGAAGGACAGGTGGTGACCGGTGCCG  
 Y A I R G Q A R V Q I V N E E G N S V F D G V L Q E G Q V V T V P  
  
 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600  
 CAGAACTTCGCGGTGGTAAAGAGATCCAGAGCCGAGAGGTTTGAGTGGTGGCGTTCAAGACCAACGACACGCGGATGGTGAACTCGCTAGCCGGGAGGA  
 Q N F A V V K R S Q S E R F E W V A F K T N D N A M V N S L A G R  
  
 3610 3620 3630 3640 3650 3660 3670 3680 3690 3700  
 CATCGGAGTAAGGGCGATCCCGCGGATGTACTGGCTAACGCCCTGGAGGTGTCCCGGAGGAGCGAGGAGGTGAAGTTCAACAGGCAGGAGACTCA  
 T S A V R A I P A D V L A N A W R V S P E E A R R V K F N R Q E T H  
  
 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800  
 CTTGGCTAGCACCCAGGGCCAGTCCAGGTCCGCCCGGAGGTTGAATGTCGTCAAGGAGGTGATCAACTTGCTTATGTAAaatgtgacggtgaaataataa  
 L A S T R G Q S R S P G R L N V V K E V I N L L M \*  
  
 3810 3820 3830 3840 3850 3860 3870 3880 3890 3900  
 cggtaaaatatatgtaataataataataaaagccaaagtgagaatgaggggaaagtgtgtaatgagccagtagcgggtggtgtaattttg  
  
 3910 3920 3930 3940 3950 3960 3970 3980 3990 4000  
 tatcgtattgtcaataaatcatgaattttgtggttttttatgtgttttttaaatcatgaatttttaaaattttataaaataatctccaatcggagaacaac  
  
 4010 4020 4030 4040 4050 4060 4070 4080 4090 4100  
 attccatatccatggatgtttctttaccctaaatctagtctttgagaggatgaagcatcaccggaacagttctgcaactatccctcaaaagctttaaaatga  
  
 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200  
 acaacaagggaacagagcaacgttccaaagatccccaaacgaaacatatattatctataactataattattattactactgcccgggaatcaccaatccct

FIGURE 4-5

4210 4220 4230 4240 4250 4260 4270 4280 4290 4300  
gaatgattcctattaactacaagccttgttgccggcgagaaagtgatcgccggcgactcgagacgagcccttgatgagcagagtc

4310 4320 4330 4340 4350 4360 4370 4380 4390 4400  
tttacctgccaggcggtgaagggaagagcgccctcttgagtaggagttcagcaagcgggttccttgccggagtaagcggaacgcaagggtggtgtc

4410 4420 4430 4440 4450 4460 4470 4480 4490 4500  
gacgtctcgtttcnggaggcgnattcatgaagggttaaaagtcanaatctcagtgctcagggagccnaaagacgttgggaaaccgtcgcncgt

4510 4520 4530 4540 4550 4560 4570 4580 4590 4600  
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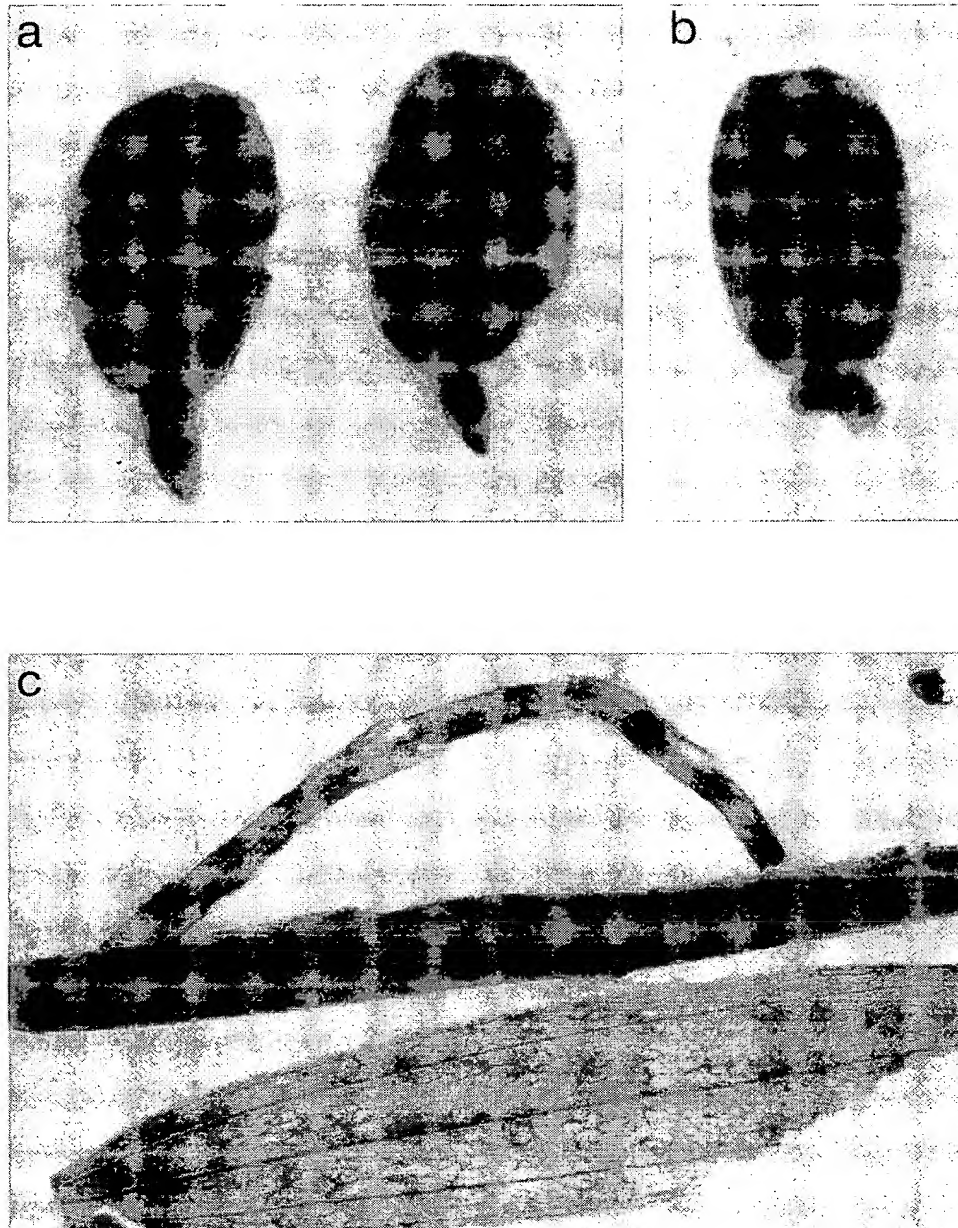
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4710 4720 4730 4740 4750 4760 4770 4780 4790 4800  
gaggnttcannngnaggagaaaaaggannccatttnannangcngaggagacatgaancggtacngagctgnggttcannnancggcgnnnngnagtcc

4810 4820 4830 4840 4850 4860 4870 4880 4890 4900  
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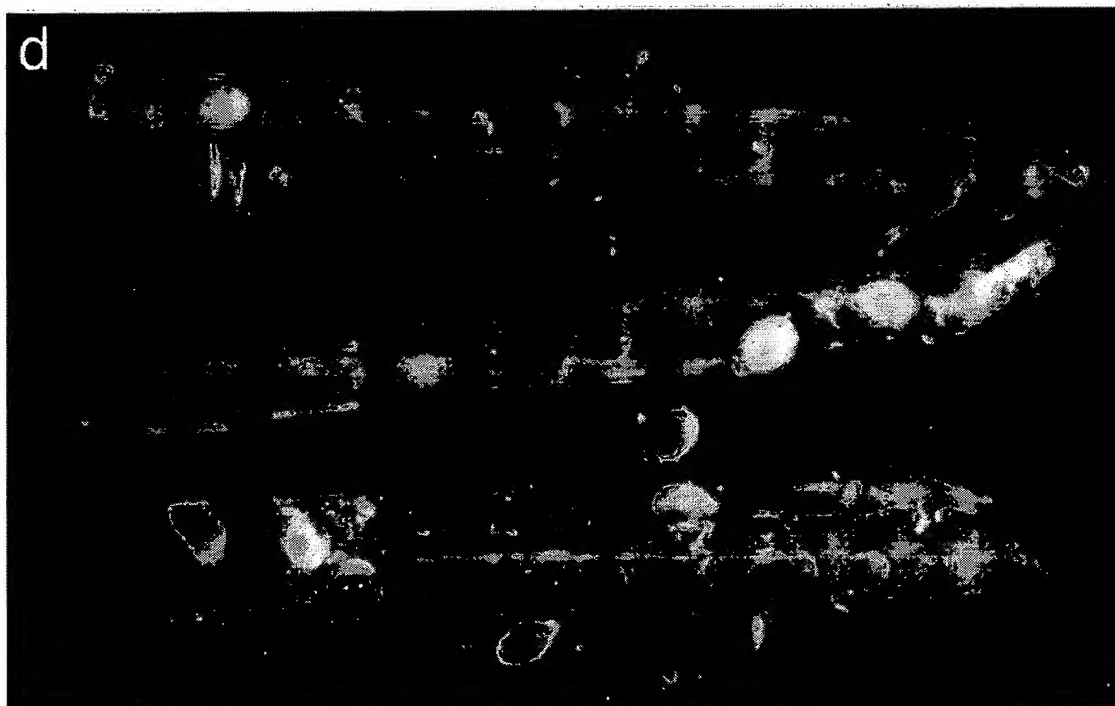
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Figure 9.1



005280" E6554960

Figure 9.2



005280" E1654960

1 ttcaaaacccgattccccgaggcgccctattgaagatatgggggaagttcgacgagatcgatgctgggtcgagtctatg 80

81 gtgatggtgccgtttgggggaggatgagcgagatagccaagactagcattccgttccacacagagttgggaatttgta 160

161 ccaatccaacacttgcgtattgagcgacgatagggacgcggaacacacatccgttggatcagggagttgtacgatg 240

241 atctcgagccttatgtgcgaagaatccgagggtatgcttacgtgaactacagggatctcgacatcgggatgaatggagga 320

321 ggtgaaggggatgagaagggtactttatggtgaggttaagggtggtggggaagtactttgggtcaactttgatcggtt 400

401 ggttcgggtgaagacgattggtgatcccaataatgtgttctcgaaacgagcagagcattccctcaattccaactcggttat 480

481 aaggatcaatgatcaatgagaatttctcttcccaatgtgattacaagttctattgggtcagctttctcaactgctcctat 560

561 tcatttagattaattcataacaactatttaattaccagccttttatccggccggttgccgatttattttcttaagtttt 640

641 agatgaaatgaaaccgattttagtttttattgagatgagattaatcttaatttgcttgaaatttactcacggttgatgtga 720

721 tatttggaaattaactaaaatgataaataatcggtataaaaaataataatttaaaataaaataacataagaacaata 800

801 aaataaaataatttaattttatcttctgttttctgtatcatacatctcttcttacttctttaaaggctt 880

881 ttcaattatcacttaattaaatacaatagataaaatcgtttaattctataaacattaaacctatacacacttgcacggtgaacaat 960

961 caatatgataataataataataataattcaattatttaattataaaatttttaattataaagtttatcggtcagtt 1040

1041 tctgcaagctccgagctccttgatcgttttagtttctgcggtctcaagggtataacgactcggagcgacgagccctttgct 1120

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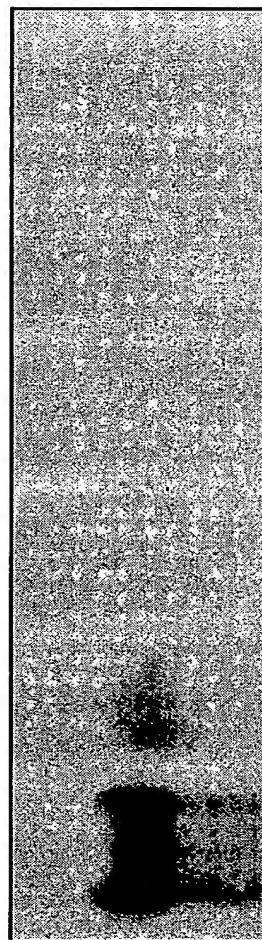
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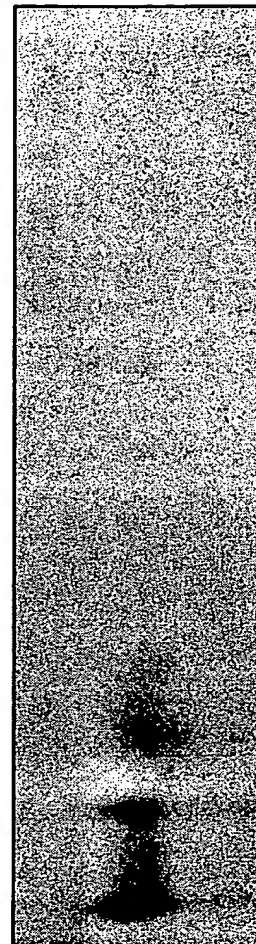
FIGURE 6

E S F L C R



H-isoform  
(3T)

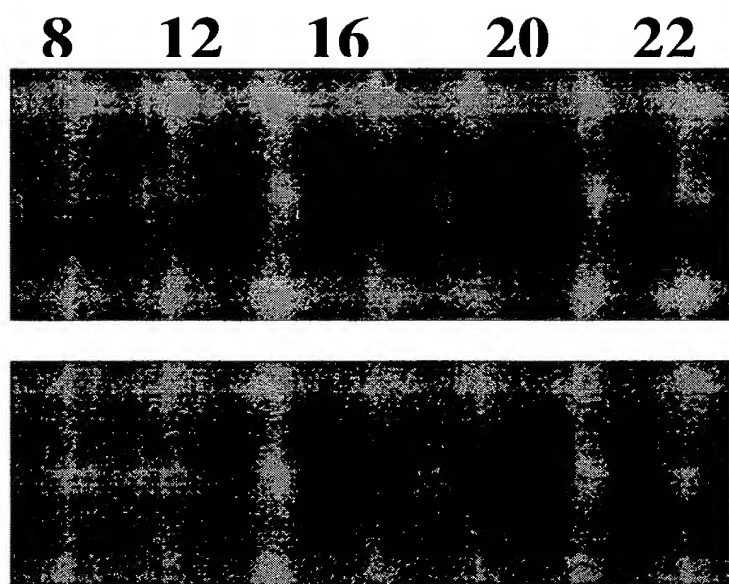
A



L-isoform  
(10J)

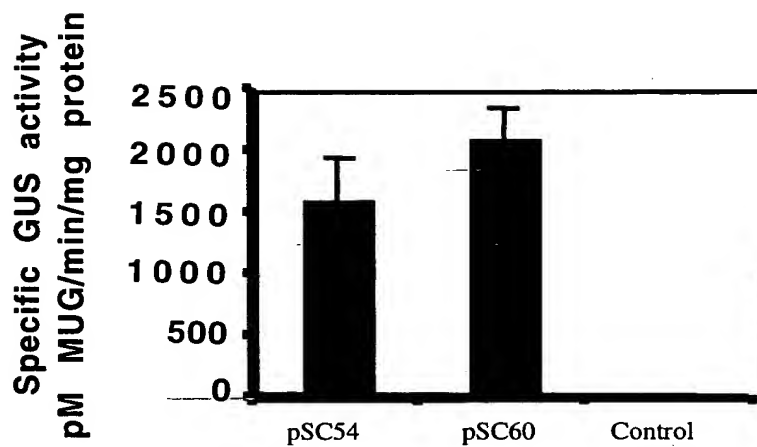
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**FIGURE 7**



005230" 665549150

FIGURE 8



005230" E654960

FIGURES 9A-C

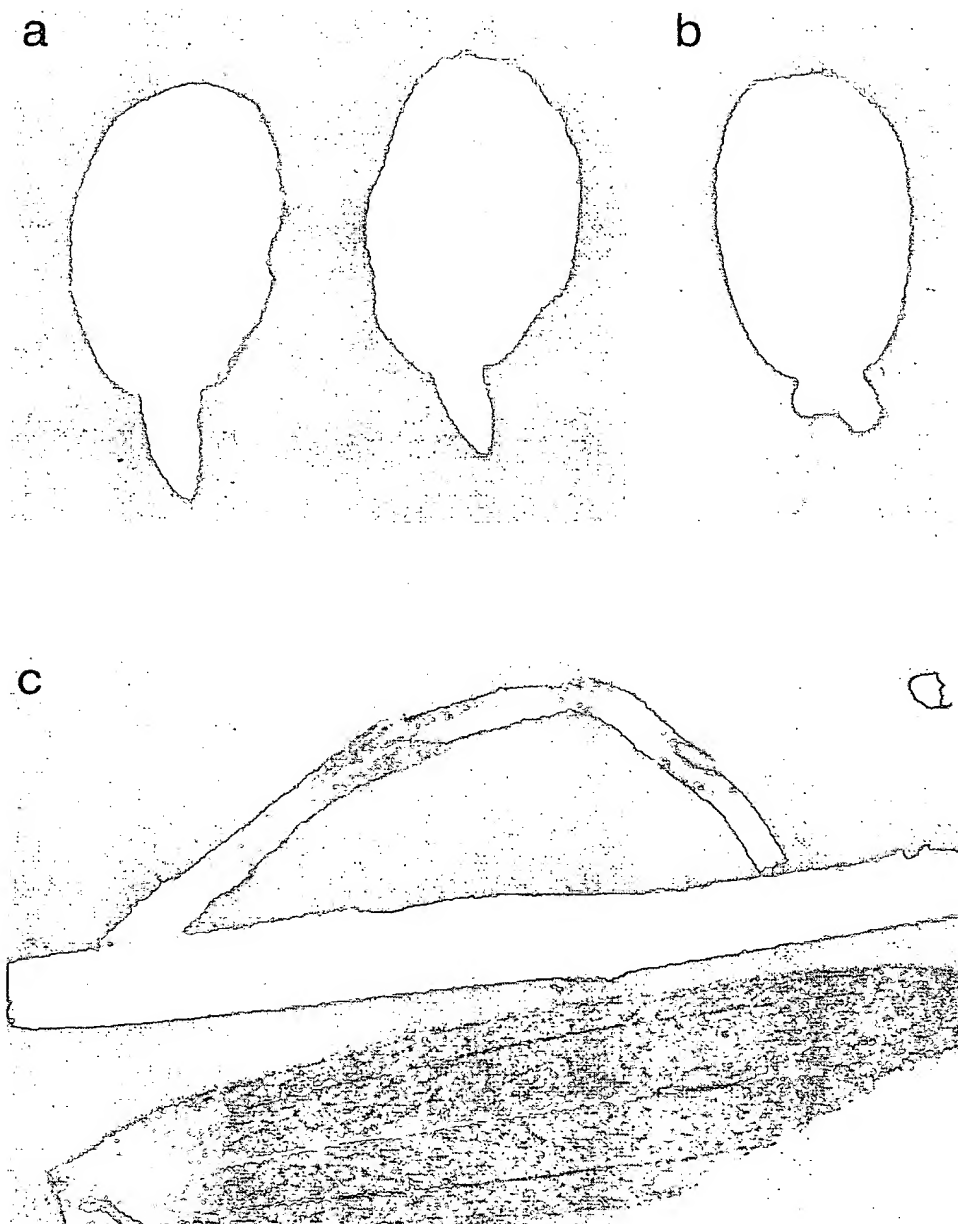
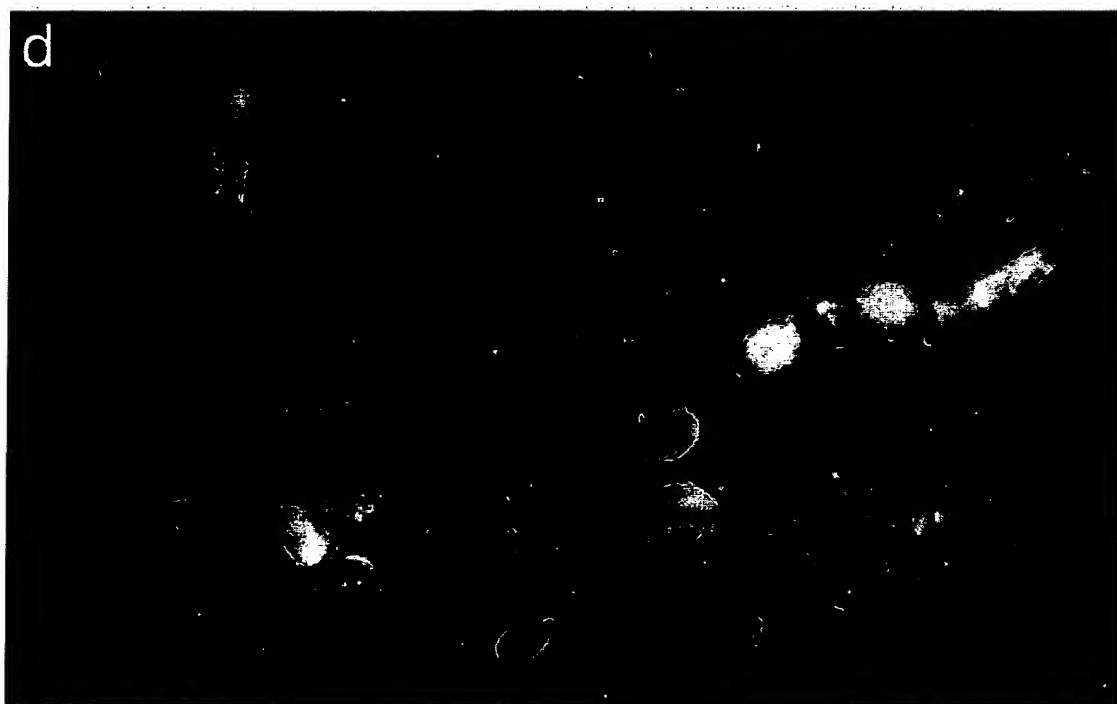


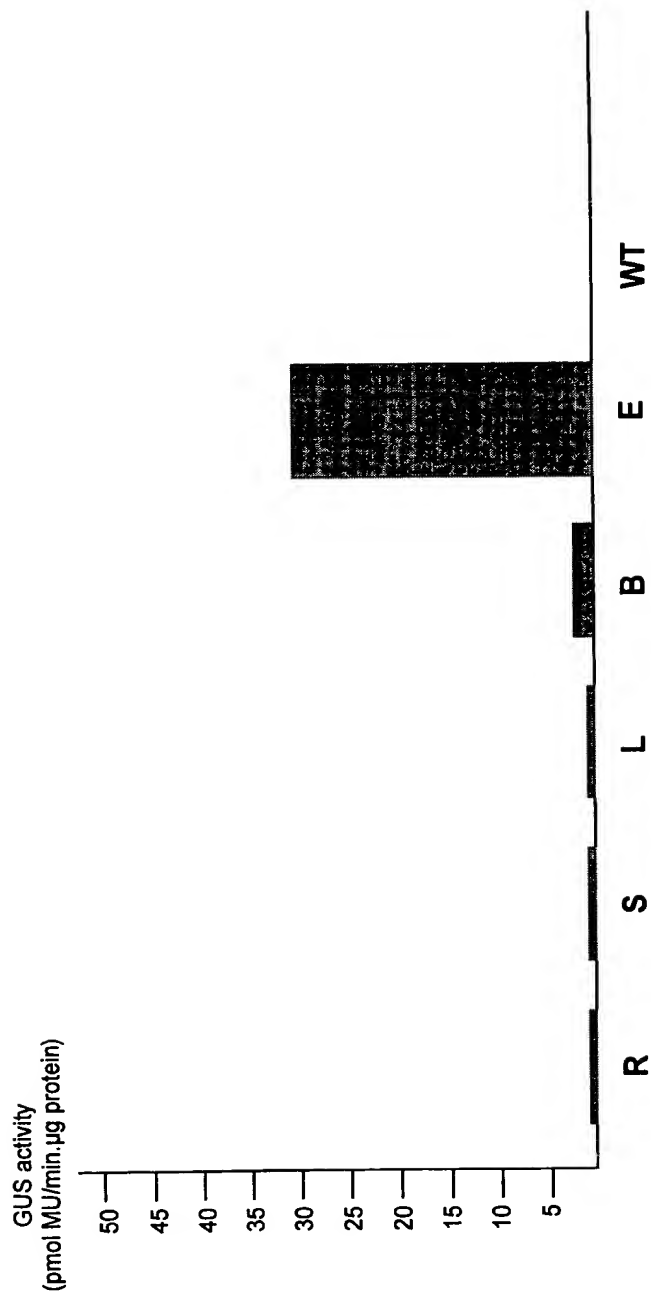
FIGURE 9D



005280" E6554960

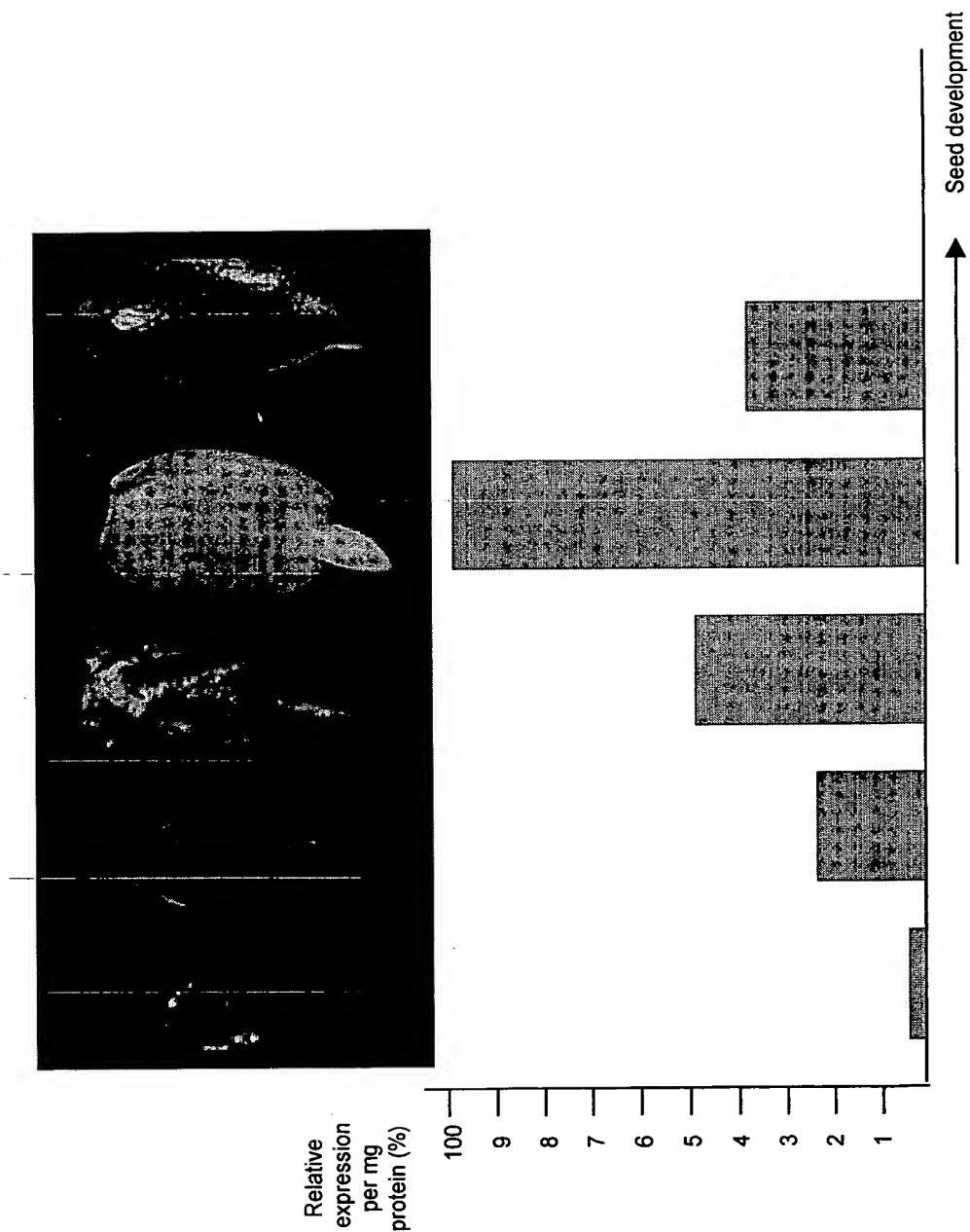
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SUBCLASS  
AFIS 100

FIGURE 10



005230" E6554960

FIGURE 11



**FIGURE 12**

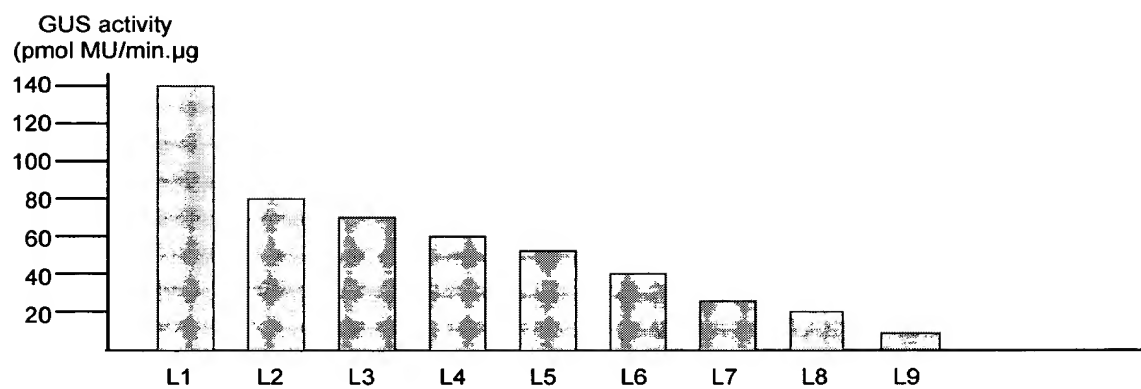


FIGURE 13

